

SEQUENCE LISTING

<110> Wright, David A.
Voytas, Daniel F.

<120> Plant Retroelements and Methods Related Thereto

<130> P-1065 ISURF Plant Retroelement

<140> unknown

<141> 1999-05-28

<150> 60/087125

<151> 1998-05-29

<160> 42

<170> PatentIn Ver. 2.0

<210> 1

<211> 18

<212> DNA

<213> Glycine max

<400> 1

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18

<210> 2

<211> 18

<212> DNA

<213> Glycine max

<400> 2

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<210> 3

<211> 6

<212> DNA

<213> Glycine max

<400> 3

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6

<210> 4

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: plant
retroelement sequence

<400> 4

Met Ala Ser Arg Lys Arg Lys

1

5

<210> 5

<211> 1263

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: plant
retroelement sequence

<400> 5

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<210> 6

<211> 421

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: plant
retroelement sequence

<400> 6

Met Ala Ser Arg Lys Arg Lys Ala Val Pro Thr Pro Gly Glu Ala Ser

1

5

10

15

Asn Trp Asp Ser Ser Arg Phe Thr Phe Glu Ile Ala Trp His Arg Tyr
 20 25 30
 Gln Asp Ser Ile Gln Leu Arg Asn Ile Leu Pro Glu Arg Asn Val Glu
 35 40 45
 Leu Gly Pro Gly Met Phe Asp Glu Phe Leu Gln Glu Leu Gln Arg Leu
 50 55 60
 Arg Trp Asp Gln Val Leu Thr Arg Leu Pro Glu Lys Trp Ile Asp Val
 65 70 75 80
 Ala Leu Val Lys Glu Phe Tyr Ser Asn Leu Tyr Asp Pro Glu Asp His
 85 90 95
 Ser Pro Lys Phe Trp Ser Val Arg Gly Gln Val Val Arg Phe Asp Ala
 100 105 110
 Glu Thr Ile Asn Asp Phe Leu Asp Thr Pro Val Ile Leu Ala Glu Gly
 115 120 125
 Glu Asp Tyr Pro Ala Tyr Ser Gln Tyr Leu Ser Thr Pro Pro Asp His
 130 135 140
 Asp Ala Ile Leu Ser Ala Leu Cys Thr Pro Gly Gly Arg Phe Val Leu
 145 150 155 160
 Asn Val Asp Ser Ala Pro Trp Lys Leu Leu Arg Lys Asp Leu Met Thr
 165 170 175
 Leu Ala Gln Thr Trp Ser Val Leu Ser Tyr Phe Asn Leu Ala Leu Thr
 180 185 190
 Phe His Thr Ser Asp Ile Asn Val Asp Arg Ala Arg Leu Asn Tyr Gly
 195 200 205
 Leu Val Met Lys Met Asp Leu Asp Val Gly Ser Leu Ile Ser Leu Gln
 210 215 220
 Ile Ser Gln Ile Ala Gln Ser Ile Thr Ser Arg Leu Gly Phe Pro Ala
 225 230 235 240
 Leu Ile Thr Thr Leu Cys Glu Ile Gln Gly Val Val Ser Asp Thr Leu
 245 250 255
 Ile Phe Glu Ser Leu Ser Pro Val Ile Asn Leu Ala Tyr Ile Lys Lys
 260 265 270
 Asn Cys Trp Asn Pro Ala Asp Pro Ser Ile Thr Phe Gln Gly Thr Arg
 275 280 285

Arg Thr Arg Thr Arg Ala Ser Ala Ser Ala Ser Glu Ala Pro Leu Pro
290 295 300

Ser Gln His Pro Ser Gln Pro Phe Ser Gln Arg Pro Arg Pro Pro Leu
305 310 315 320

Leu Ser Thr Ser Ala Pro Pro Tyr Met His Gly Gln Met Leu Arg Ser
325 330 335

Leu Tyr Gln Gly Gln Gln Ile Ile Ile Gln Asn Leu Tyr Arg Leu Ser
340 345 350

Leu His Leu Gln Met Asp Leu Pro Leu Met Thr Pro Glu Ala Tyr Arg
355 360 365

Gln Gln Val Ala Lys Leu Gly Asp Gln Pro Ser Thr Asp Arg Gly Glu
370 375 380

Glu Pro Ser Gly Ala Ala Ala Thr Glu Asp Pro Ala Val Asp Glu Asp
385 390 395 400

Leu Ile Ala Asp Leu Ala Gly Ala Asp Trp Ser Pro Trp Ala Asp Leu
405 410 415

Gly Arg Gly Ser Glx
420

<210> 7

<211> 1596

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: plant
retroelement sequence

<400> 7

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acactagagg acttctctaa taccaccact cctcagttct ttacaagtat cacaaggccg 240
gaagtccaag cagatctcct tactcaaggg aacctcttcc atggtcttcc aaatgaagat 300
ccatatgcgc atctagcctc atacatagag atatgcagca ccgttaaaat cgccggagtt 360
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tggttgcaat cctttaaagg caatagctta agaacatggg aagaagtagt ggaaaaattc 480
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catcaatttc tggatgaatc ccttagcgaa gcactagacc atttccacgg attgctaaga 600
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caactcttaa tcgaaacagc tactagaggg aagatcaagc tgaagactcc cgaagaagcg 720

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```

<210> 8

<211> 532

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: plant
retroelement sequence

<400> 8

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Met Arg Gly Arg Thr Ala Ser Gly Asp Val Val Pro Ile Asn Leu Glu
  1             5             10             15

```

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Ile Glu Ala Thr Cys Arg Arg Asn Asn Ala Ala Arg Arg Arg Arg Glu
      20             25             30

```

```

Gln Asp Ile Glu Gly Ser Ser Tyr Thr Ser Pro Pro Pro Ser Pro Asn
      35             40             45

```

```

Tyr Ala Gln Met Asp Gly Glu Pro Ala Gln Arg Val Thr Leu Glu Asp
      50             55             60

```

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Phe Ser Asn Thr Thr Thr Pro Gln Phe Phe Thr Ser Ile Thr Arg Pro
      65             70             75             80

```

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Glu Val Gln Ala Asp Leu Leu Thr Gln Gly Asn Leu Phe His Gly Leu
      85             90             95

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```

Pro Asn Glu Asp Pro Tyr Ala His Leu Ala Ser Tyr Ile Glu Ile Cys
      100            105            110

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```

Ser Thr Val Lys Ile Ala Gly Val Pro Lys Asp Ala Ile Leu Leu Asn
      115            120            125

```

```

Leu Phe Ser Phe Ser Leu Ala Gly Glu Ala Lys Arg Trp Leu His Ser

```

130		135		140
Phe Lys Gly Asn Ser Leu Arg Thr Trp Glu Glu Val Val Glu Lys Phe				
145		150		155
Leu Lys Lys Tyr Phe Pro Glu Ser Lys Thr Val Glu Arg Lys Met Glu				
	165		170	175
Ile Ser Tyr Phe His Gln Phe Leu Asp Glu Ser Leu Ser Glu Ala Leu				
	180		185	190
Asp His Phe His Gly Leu Leu Arg Lys Thr Pro Thr His Arg Tyr Ser				
	195		200	205
Glu Pro Val Gln Leu Asn Ile Phe Ile Asp Asp Leu Gln Leu Leu Ile				
	210		215	220
Glu Thr Ala Thr Arg Gly Lys Ile Lys Leu Lys Thr Pro Glu Glu Ala				
	225		230	235
Met Glu Leu Val Glu Asn Met Ala Ala Ser Asp Gln Ala Ile Leu His				
	245		250	255
Asp His Thr Tyr Val Pro Thr Lys Arg Ser Leu Leu Glu Leu Ser Thr				
	260		265	270
Gln Asp Ala Thr Leu Val Gln Asn Lys Leu Leu Thr Arg Gln Ile Glu				
	275		280	285
Ala Leu Ile Glu Thr Leu Ser Lys Leu Pro Gln Gln Leu Gln Ala Ile				
	290		295	300
Ser Ser Ser His Ser Ser Val Leu Gln Val Glu Glu Cys Pro Thr Cys				
	305		310	315
Arg Gly Thr His Glu Pro Gly Gln Cys Ala Ser Gln Gln Asp Pro Ser				
	325		330	335
Arg Glu Val Asn Tyr Ile Gly Ile Leu Asn Arg Tyr Gly Phe Gln Gly				
	340		345	350
Tyr Asn Gln Gly Asn Pro Ser Gly Phe Asn Gln Gly Ala Thr Arg Phe				
	355		360	365
Asn His Glu Pro Pro Gly Phe Asn Gln Gly Arg Asn Phe Met Gln Gly				
	370		375	380
Ser Ser Trp Thr Asn Lys Gly Asn Gln Tyr Lys Glu Gln Arg Asn Gln				
	385		390	395
Pro Pro Tyr Gln Pro Pro Tyr Gln His Pro Ser Gln Gly Pro Asn Gln				

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: plant
retroelement sequence

<400> 10

Cys Asp Lys Cys Gln Arg Thr Gly Gly Ile Ser Arg Arg Asn Glu Met
1 5 10 15

Pro Leu Gln Asn Ile Met Glu Val Glu Ile Phe Asp Cys Trp Gly Ile
20 25 30

Asp Phe Met Gly Pro Phe Pro Ser Ser Tyr Gly Asn Val Tyr Ile Leu
35 40 45

Val Ala Val Asp Tyr Val Ser Lys Trp Val Glu Ala Ile Ala Thr Pro
50 55 60

Lys Asp Asp Ala Arg Val Val Ile Lys Phe Leu Lys Lys Asn Ile Phe
65 70 75 80

Ser Arg Phe Gly Val Pro Arg Ala Leu Ile Ser Asp Arg Gly Thr His
85 90 95

Phe Cys Asn Asn Gln Leu Lys Lys Val Leu Glu His Tyr Asn Val Arg
100 105 110

His Lys Val Ala Thr Pro Tyr His Pro Gln Thr Asn Gly Gln Ala Glu
115 120 125

Ile Ser Asn Arg Glu Leu Lys Arg Ile Leu Glu Lys Thr Val Ala Ser
130 135 140

Thr Arg Lys Asp Trp Ser Leu Lys Leu Asp Asp Ala Leu Trp Ala Tyr
145 150 155 160

Arg Thr Ala Phe Lys Thr Pro Ile Gly Leu Ser Pro Phe Gln Leu Val
165 170 175

Tyr Gly Lys Ala Cys His Leu Pro Val Glu Leu Glu Tyr Lys Ala Tyr
180 185 190

Trp Ala Leu Lys Leu Leu Asn Phe Asp
195 200

<210> 11

<211> 600

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: plant
retroelement sequence

<400> 11

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cgaactgtca ctggttggcg aatgtgtatc gactatcgca agctgaatga agccacacgg 180
aaggaccatt tccccttacc ttcatggat cagatgctgg agagacttgc agggcaggca 240
tactactgtt tcttgatgg atactcggga tacaaccaga tcgcggtaga cccagagat 300
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gtggagaaaa gcatcgaggt atttatggac gacttctcgg tttttggacc ctcatttgac 480
agctgtttga ggaacctaga gagggactt cagagggtgcg aagagactaa cttggtactg 540
aattgggaaa agtgtcattt catggttcga gagggcatag tcctaggcca caagatctca 600
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<210> 12

<211> 200

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: plant
retroelement sequence

<400> 12

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Leu Glu Ala Gly Leu Ile Tyr Pro Ile Ser Asp Ser Ala Trp Val Ser
 1             5             10             15

Pro Val Gln Val Val Pro Lys Lys Gly Gly Met Thr Val Val Arg Asp
 20             25             30

Glu Arg Asn Asp Leu Ile Pro Thr Arg Thr Val Thr Gly Trp Arg Met
 35             40             45

Cys Ile Asp Tyr Arg Lys Leu Asn Glu Ala Thr Arg Lys Asp His Phe
 50             55             60

Pro Leu Pro Phe Met Asp Gln Met Leu Glu Arg Leu Ala Gly Gln Ala
 65             70             75             80

Tyr Tyr Cys Phe Leu Asp Gly Tyr Ser Gly Tyr Asn Gln Ile Ala Val
 85             90             95

Asp Pro Arg Asp Gln Glu Lys Thr Ala Phe Thr Cys Pro Phe Gly Val
100             105             110

Phe Ala Tyr Arg Arg Met Pro Phe Gly Leu Cys Asn Ala Pro Ala Thr
```

115	120	125
Phe Gln Arg Cys Met Leu Ala Ile Phe Ser Asp Met Val Glu Lys Ser		
130	135	140
Ile Glu Val Phe Met Asp Asp Phe Ser Val Phe Gly Pro Ser Phe Asp		
145	150	155
Ser Cys Leu Arg Asn Leu Glu Arg Val Leu Gln Arg Cys Glu Glu Thr		
165	170	175
Asn Leu Val Leu Asn Trp Glu Lys Cys His Phe Met Val Arg Glu Gly		
180	185	190
Ile Val Leu Gly His Lys Ile Ser		
195	200	

<210> 13
 <211> 858
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: plant
 retroelement sequence

<400> 13
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 ccattcgggg aagccttaca gcagatgccc ctctactcca aatttatgaa agacatcctc 180
 accaagaagg ggaagtatat tgacaacgag aatattgtgg taggaggcaa ttgcagtgcg 240
 ataatacaaaa ggattctacc caagaagttt aaagaccccg gaagtgttac catcccgtgc 300
 accattggga aggaagccgt aaacaaggcc ctcatgtatc taggagcaag tatcaatctg 360
 atgcccttgt caatgtgcaa aagaattggg aatttgaaga tagatccac caagatgacg 420
 cttcaactgg cagaccgctc aatcacaagg ccatatgggg tggtagaaga tgccttggtc 480
 aaggtagccc acttcacttt tccggtggac tttgttatca tggatatcga agaagacact 540
 gagattcccc ttatcttagg cagacccttc atgctgactg ccaactgtgt ggtggatatg 600
 gggaaaggga acttagagtt gactattgat aatcagaaga tcaccttga ctttatcaag 660
 gcaatgaagt acccacagga gggttggaag tgcttcagaa tagaggagat tgatgaggaa 720
 gatgtcagtt ttctcgagac accaaagact tcgctagaaa aagcaatggg aaatcattta 780
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<210> 14
 <211> 286
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: plant

retroelement sequence

<400> 14

Lys Glu Glu Pro Leu Ala Leu Pro Gln Asp Leu Pro Tyr Pro Met Ala
1 5 10 15

Pro Thr Lys Lys Asn Lys Glu Arg Tyr Phe Ala Arg Phe Leu Glu Ile
20 25 30

Phe Lys Gly Leu Glu Ile Thr Met Pro Phe Gly Glu Ala Leu Gln Gln
35 40 45

Met Pro Leu Tyr Ser Lys Phe Met Lys Asp Ile Leu Thr Lys Lys Gly
50 55 60

Lys Tyr Ile Asp Asn Glu Asn Ile Val Val Gly Gly Asn Cys Ser Ala
65 70 75 80

Ile Ile Gln Arg Ile Leu Pro Lys Lys Phe Lys Asp Pro Gly Ser Val
85 90 95

Thr Ile Pro Cys Thr Ile Gly Lys Glu Ala Val Asn Lys Ala Leu Ile
100 105 110

Asp Leu Gly Ala Ser Ile Asn Leu Met Pro Leu Ser Met Cys Lys Arg
115 120 125

Ile Gly Asn Leu Lys Ile Asp Pro Thr Lys Met Thr Leu Gln Leu Ala
130 135 140

Asp Arg Ser Ile Thr Arg Pro Tyr Gly Val Val Glu Asp Val Leu Val
145 150 155 160

Lys Val Arg His Phe Thr Phe Pro Val Asp Phe Val Ile Met Asp Ile
165 170 175

Glu Glu Asp Thr Glu Ile Pro Leu Ile Leu Gly Arg Pro Phe Met Leu
180 185 190

Thr Ala Asn Cys Val Val Asp Met Gly Lys Gly Asn Leu Glu Leu Thr
195 200 205

Ile Asp Asn Gln Lys Ile Thr Phe Asp Leu Ile Lys Ala Met Lys Tyr
210 215 220

Pro Gln Glu Gly Trp Lys Cys Phe Arg Ile Glu Glu Ile Asp Glu Glu
225 230 235 240

Asp Val Ser Phe Leu Glu Thr Pro Lys Thr Ser Leu Glu Lys Ala Met
245 250 255

Val Asn His Leu Asp Cys Leu Thr Ser Glu Glu Glu Glu Asp Leu Lys
 260 265 270

Ala Cys Leu Glu Asn Leu Asp Gln Glu Asp Ser Ile Pro Glu
 275 280 285

<210> 15
 <211> 192
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: plant
 retroelement sequence

<400> 15
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 tatgcaacca cagaaaagga gatgctagcc attgtctttg ccttggagaa gttcaggtca 180
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<210> 16
 <211> 64
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: plant
 retroelement sequence

<400> 16
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 1 5 10 15

Gly Gln Arg Lys Asp Lys Val Phe His Ala Ile Tyr Tyr Ala Ser Lys
 20 25 30

Val Leu Asn Glu Ala Gln Leu Asn Tyr Ala Thr Thr Glu Lys Glu Met
 35 40 45

Leu Ala Ile Val Phe Ala Leu Glu Lys Phe Arg Ser Tyr Leu Ile Gly
 50 55 60

<210> 17
 <211> 12286

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: plant
retroelement sequence

<400> 17

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retroelement sequence

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Gln Asp Ile Glu Gly Ser Ser Tyr Thr Ser Pro Pro Pro Ser Pro Asn
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```

Tyr Ala Gln Met Asp Gly Glu Pro Ala Gln Arg Val Thr Leu Glu Asp
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Phe Ser Asn Thr Thr Thr Pro Gln Phe Phe Thr Ser Ile Thr Arg Pro
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Glu Val Gln Ala Asp Leu Leu Thr Gln Gly Asn Leu Phe His Gly Leu
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Pro Asn Glu Asp Pro Tyr Ala His Leu Ala Ser Tyr Ile Glu Ile Cys
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Ser Thr Val Lys Ile Ala Gly Val Pro Lys Asp Ala Ile Leu Leu Asn
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Leu Phe Ser Phe Ser Leu Ala Gly Glu Ala Lys Arg Trp Leu His Ser
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Phe Lys Gly Asn Ser Leu Arg Thr Trp Glu Glu Val Val Glu Lys Phe
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 Asp His Thr Tyr Val Pro Thr Lys Arg Ser Leu Leu Glu Leu Ser Thr
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 660 665 670

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Asp Val Leu Val Lys Val Arg His Phe Thr Phe Pro Val Asp Phe Val

690

695

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Thr Glu Glu Glu Asn Arg Leu Val Asp Val Leu Lys Lys His Arg Glu
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Ala Ile Gly Trp His Ile Ser Asp Leu Lys Glu Ile Ser Pro Ala Tyr
885 890 895

Cys Met His Arg Ile Met Met Glu Glu Asp Tyr Lys Pro Val Arg Gln
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Val Leu Lys Leu Leu Glu Ala Gly Leu Ile Tyr Pro Ile Ser Asp Ser
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acacctattc	tgatagcttg	tggagtccca	ctcatttctg	ctggactcga	gccacgagca	1020
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cacaggttca	ggtttgagca	ctctacagac	aggagagcta	acatccttct	ccctagccct	1140
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cagaagtggg	gcaagaagca	ggacaggctg	atcgccaagt	gtttcaagct	tctgacagac	1440
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ggtgctggcc	gcagcagaag	gagagatgtc	gagtttctct	agagcgggtc	tggccgccac	1740
agagctgatg	aggtcgagta	cccatctgct	ggagctgata	cagaacaagg	aggttcgtct	1800
atggcctggg	agcaatcgca	ggcagccatt	gacgagcaac	tacgttcatt	cttcgac	1857

<210> 25

<211> 1254

<212> DNA

<213> *Pisum sativum*

<400> 25

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ttgaaaaagc gaaagatttt gccggaaaaag agatttataa tcaaccctga aggcacgaac 180
cgtacattcg ccgggctgat taacagcaaa aagtgggacc ggtaaatatc ccccttgaag 240
cattacgaca tcgcaacagt gcgtgagttc tacgcgaacg cactgccgaa cgacgacgag 300
ccattcacat ggacgtctag agtgtccggc cgtcctgttg cgttcgatcg ggatgcaatt 360
aaccgtgtcc tgggtgaacc gctccatctg ggagccaatg agagagacac ttaccaccaa 420
gatttaaggc ttcaccggga taccgattcg atttctactg ccctgctttt ggaagggaaa 480
tcagttgagc tgaacccatc tggggttccg atgagatacc atagggagga catgattccc 540
ttggctcaac tgatcctttt gttggttcct acaaacatca aaccaagtc tcacacttct 600
accgtgccga tcccagtggc acacttggtg cacatcatcc tcacgaatat ccagattgat 660
gtggcaagga ttattgcttt ggagttgaag tccgtgattg aaagcgggct aaagtcgggg 720
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```

<210> 26

<211> 564

<212> DNA

<213> *Arabidopsis thaliana*

<400> 26

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atcttggaag ttgagatctt tgatgtatgg gggattgatt ttatgggtcc attcccatct 120
tcatacggta ataaatatat actggctgcc gtagactacg tatcaaagtg ggtcgaagct 180
attgctagtc ctaccaacga tgcaaaagtt gtgctgaagt tgttcaaaac cataatcttc 240
ccaagatttg gagttccag ggtagtaatc agtgatggcg gaaagcattt catcaacaag 300
gtttttgaga acctcttgaa gaagcatggg gtaaagcagg ttgagatctc caatagggag 360
ataaaaacaa ttctggaaaa gactgttggg attacaagga aagactggtc tgcaaagcta 420
gatgatgcat tatgggctta caggacagct ttcaagacct ccataggtac aactcctttc 480
aatcttctct atggaaaatt atgtcatcta cccgttgagc tcgagtacaa agcaatgtgg 540
gcggtaaaac ttctgaactt tgac 564
```

<210> 27

<211> 600

<212> DNA

<213> *Arabidopsis thaliana*

<400> 27

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cttgatgctg gtgtcatcta ccctatctct gatagtactt gggtttctcc agtgcattgc 60
gtccctaaaa aggggtggaat gactgttgtc aaaaatgaaa aagatgaact gatccctact 120
```

```

agaactataa ctggtcataa aatgtgcata gattatagga agttgaacgc tgcattctagg 180
aaagatcatt ttcttttacc attcattgac caaatgcttg aacgtttggc taatcatcca 240
tattattgct ttcttgatgg atacagtggg ttctttcaaa taccaattca ccctaattgat 300
caagaaaaaa ccaactttcac gtgtccttat ggaacttttg cctataaaaag aatgccattt 360
ggtttatgca atgctcctgc aacatttcag aggtgtatga cctctatatt ttcagactta 420
atcgaggaga tgggtggagg ttcatgggac gatttttcgg tctatggccc ctctttctcc 480
tcatgtttgt tgaatcttgg cagggtattg actaggtgcg aagagacgaa tcttggttctc 540
aattgggaaa agtgtcattt catggtgaag gaaggcatag tattggacca caagatatca 600

```

<210> 28

<211> 192

<212> DNA

<213> *Arabidopsis thaliana*

<400> 28

```

tttgaaatca tgtgtgatgc atcagattac gcagtaggag ctgttctagg ccagaaaata 60
gacaagaagc ttcatgtcat atattacgcc agccgaacgt tggatgacgc tcagggaaga 120
tatgcaacaa ctgagaagga gcttctagct gttgtattcg catttgagaa gttcagaagc 180
tatttggttg ga 192

```

<210> 29

<211> 597

<212> DNA

<213> *Pisum sativum*

<400> 29

```

ttggatgcca gaatgattta cccgatctcg gatagtcctat gggtcagtcc cgtgcatgtg 60
gttccgaaga aagggtgaaa taccgtcatc cggaatgaca aggatgaatt gatccctacc 120
aaagttgcaa cggggtggag aatgtgtatt gaatataggc gggtgaatac cgcaactcga 180
aaggaccatt ttccactccc gttcatggat caaatgctgg aaagactctc cgggcaacaa 240
tactattgtt tcttgatgg ctattccggg tataacccaaa ttgccgttga cccggccgat 300
cattaaaaga cggctttcac atgtccggtt ggagtgttcg cataccgaaa aatgtccttt 360
gggttgatga atgcaccgac gactttccaa cgatgtgtgc aagccatttt tgccgacctt 420
aatgagaaaa caatggaagt cttcatggat gacttctcgg tatttggtgt atcctttagt 480
ttatgcttgg caaacttgaa aacgggtgctt gaaagatgtg tgaagaccaa tcttggtgctt 540
aattggtaga agtgccactt catggtgacc gaggggatag tgcttgcca taaagtc 597

```

<210> 30

<211> 192

<212> DNA

<213> *Pisum sativum*

<400> 30

```

tttgagctaa tgtgtgatgc gagcaactat gcaatcggag cgggtattagg ccaaagaaaa 60
gagaaaaaat ttcatgcgat acattacgca agtaaagttc ttaatgaggc tcaaattaac 120
tatgccacca ctgaaaaaga attacttgcg atagtgtatg cacttgaaaa gtttaggtct 180
tatcttatag gg 192

```

<210> 31

<211> 581

<212> DNA

<213> Pisum sativum

<400> 31

```
tgtgatagtt gccagagaag cgggtgggatt ggtaagagag acgagatgtc tctccaaaac 60
atccaagagg tcgaagtatt tgattgttgg ggcacgcatt ttgtaggacc attccccctt 120
cttatggtaa cgagtatatg cttgtcgcag ttgaggcgat tgcctcacct cgggcgggatg 180
cgaaaacggg aataatTTTT ttgaagaaaa acatatTTTt ccgTTTcggg accccccgag 240
tgTTgataag tgacggaggg tcacactTTT gtaatgcacc gTTggaaagc attTTaaaac 300
attacggTgt atcacacaga gtggcaactc cgtatcacc acaggctaag ggacaagccg 360
aggTctctaa tcgtgagatt aagagaattc tcgaaaaaac tgtgtcaaat tcgaaaaaag 420
agtggTcaca aaaattggat gaagcgTtat gggcataccg taccgccttt aaagctccaa 480
ttgggtcac tcctTTTcaa ttgggtTTTg gtaaaaactg ccatttgcg gtcgaattgg 540
agcacaaagc cttgtgggct ttgaaaatta ataattTTTga a 581
```

<210> 32

<211> 1362

<212> DNA

<213> Glycine max

<400> 32

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tcacgtTTTca cTTTcgagat tgcttggcac agataccagg atagcattca gTccggaaac 120
atcctTccag agaggaatgt agagcttggg ccagggatgt ttgatgagtt cctgcaggaa 180
ctccagaggc tcagatggga ccaggTtctg acccgacttc cagagaagtg gattgatgtt 240
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cctccagacc atgatgccat cctTtccgct ctgtgtactc caggggggacg atttgttctg 480
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gacagggccc gactcaatta tggcttggTg atgaagatgg acctggacgt gggcagcctc 660
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tgatcttatg cTttaatgtt tTctTTTata ttatgtTtTg gTtctctTTt atgtTttatg 1320
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```

<210> 33

<211> 192

<212> DNA

<213> Glycine max

<400> 33

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```

ggcaaaat ttcattgctat ctactacgcc agcaaagttt taaatgatgc acagggttaac 120

tatgctacca cagaaaaaga aatgttggca attgtttatg cacttgaaaa gttcaaattct 180
tatttggtag gc 192

<210> 34

<211> 597

<212> DNA

<213> Glycine max

<400> 34

ttggagggtt ggctcatata ccccatctct gacaacgctt gggtaagccc agtacagggtg 60
gttcccaaga aagggtggaat gacagtggta caaaatgaga ggaatgactt gataccaaca 120
cgaacagtca ctggctggcg aatgtgtatt gactatcaca agctgaatga agctacacgg 180
aaggaccatt tccccctacc ttcatggat cagatgctgg agagacttgc agggcaggca 240
tactactgtt tcttggatgg atactcggga tacaaccaga tcgcggtaga ccccatagat 300
caggagaaga cggctctttac atgccccttt ggcgtctttg cttacagaag gatgtcattc 360
gggttatgta atgtaccagc cacatttcag aggtgcatgc tgaccatttt ttcagacatg 420
gtggagaaaa gcatcgaggt atttatggac gacttctcgg ttttggacc ctcatttgac 480
agctgtttga ggaacctaga aatggtactt cagagggtgc tagagactaa cttggtactg 540
aattgggaaa agtgtcattt tatggttcga gagggcatag tcctaggcca caagatc 597

<210> 35

<211> 603

<212> DNA

<213> Glycine max

<400> 35

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tcatacagga atgtctacat cttggttagct gtggattacg tctccaaatg ggtggaagcc 180
atagccacgc tgaaggacga tgccagggtta gtgatcaaat ttctgaagaa gaacattttt 240
tcccatctcg gagtcccacg agccttgatt agtcatgggg gaacgcactt ctgcaacaat 300
cagttgaaga aagtcctgga gcaactataat gtccgacaca aggtggccac acctatcac 360
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acagttgcat catcaagaaa ggattggggc ttgaagctcg atgatactct ctgggcctat 480
aggacagcgt tcaagactcc catcggctta tcaccatttc agctagtata tgggaaggca 540
tgtcatttac cagtagagct ggagcacaag gcatattggg ctctcaagtt gctcaacttt 600
gac 603

<210> 36

<211> 150

<212> DNA

<213> Glycine max

<400> 36

cctaaaatac tacaacgaca tgattggtgt tttaggataa ttgactgaaa aacctattat 60
caatttggcg ccgttgccaa ttgggtgttt gtttgttaca tttgagattt cagacttgct 120
tagatcaagt tctttttcaa ttttcttttt 150

<210> 37

<211> 11
<212> DNA
<213> Glycine max

<400> 37
tggcgccggtt g 11

<210> 38
<211> 15
<212> DNA
<213> Glycine max

<400> 38
tggcgccggtt gccgg 15

<210> 39
<211> 27
<212> DNA
<213> Glycine max

<400> 39
tttttggcgc cggtgtcggg gattttg 27

<210> 40
<211> 9
<212> DNA
<213> Glycine max

<400> 40
tttggggga 9

<210> 41
<211> 16
<212> DNA
<213> Glycine max

<400> 41
tttaatttgg gggatt 16